

#4

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/519,335
Source: Pu/10
Date Processed by STIC: 10/28/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 10/28/2005

PATENT APPLICATION: US/10/519,335

TIME: 12:21:46

Input Set : N:\RJAVED\10519335.txt

Output Set: N:\CRF4\10282005\J519335.raw

3 <110> APPLICANT: Cavarec, Laurent
 4 Chumakov, Ilya
 5 Destenaves, Benoit
 6 Gonthier, Catherine
 7 Elias, Isabelle
 9 <120> TITLE OF INVENTION: NOVEL KCNQ POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES
 IN THE
 10 TREATMENT OF MENTAL DISORDERS
 12 <130> FILE REFERENCE: G-194US03PCT
 14 <140> CURRENT APPLICATION NUMBER: US 10/519,335
 15 <141> CURRENT FILING DATE: 2004-12-22
 17 <150> PRIOR APPLICATION NUMBER: US 60/391,359
 18 <151> PRIOR FILING DATE: 2002-06-25
 20 <160> NUMBER OF SEQ ID NOS: 47
 22 <170> SOFTWARE: PatentIn version 3.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1932
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(1932)
 33 <400> SEQUENCE: 1
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 35 Met Val Gln Lys Ser Arg Asn Gly Gly Val Tyr Pro Gly Pro Ser Gly
 36 1 5 10 15
 38 gag aag aag ctg aag gtg ggc ttc gtg ggg ctg gac ccc ggc gcg ccc 96
 39 Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
 40 20 25 30
 42 gac tcc acc cgg gac ggg gcg ctg ctg atc gcc ggc tcc gag gcc ccc 144
 43 Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
 44 35 40 45
 46 aag cgc ggc agc atc ctc agc aaa cct cgc gcg ggc ggc gcg ggc gcc 192
 47 Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
 48 50 55 60
 50 ggg aag ccc ccc aag cgc aac gcc ttc tac cgc aag ctg cag aat ttc 240
 51 Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
 52 65 70 75 80
 54 ctc tac aac gtg ctg gag cgg ccg cgc ggc tgg gcg ttc atc tac cac 288
 55 Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
 56 85 90 95
 58 gcc tac gtg ttc ctc ctg gtt ttc tcc tgc ctc gtg ctg tct gtg ttt 336
 59 Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
 60 100 105 110

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62	tcc acc atc aag gag tat gag aag agc tcg gag ggg gcc ctc tac atc	384
63	Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile	
64	115 120 125	
66	ctg gaa atc gtg act atc gtg gtg ttt ggc gtg gag tac ttc gtg cgg	432
67	Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg	
68	130 135 140	
70	atc tgg gcc gca ggc tgc tgc tgc cgg tac cgt ggc tgg agg ggg cgg	480
71	Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg	
72	145 150 155 160	
74	ctc aag ttt gcc cgg aaa ccg ttc tgt gtg att gac atc atg gtg ctc	528
75	Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu	
76	165 170 175	
78	atc gcc tcc att gcg gtg ctg gcc gcc ggc tcc cag ggc aac gtc ttt	576
79	Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe	
80	180 185 190	
82	gcc aca tct gcg ctc cgg agc ctg cgc ttc ctg cag att ctg cgg atg	624
83	Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met	
84	195 200 205	
86	atc cgc atg gac cgg cgg gga ggc acc tgg aag ctg ctg ggc tct gtg	672
87	Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val	
88	210 215 220	
90	gtc tat gcc cac agc aag gag ctg gtc act gcc tgg tac atc ggc ttc	720
91	Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe	
92	225 230 235 240	
94	ctt tgt ctc atc ctg gcc tcg ttc ctg gtg tac ttg gca gag aag ggg	768
95	Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly	
96	245 250 255	
98	gag aac gac cac ttt gac acc tac gcg gat gca ctc tgg tgg ggc ctg	816
99	Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu	
100	260 265 270	
102	atc acg ctg acc acc att ggc tac ggg gac aag tac ccc cag acc tgg	864
103	Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp	
104	275 280 285	
106	aac ggc agg ctc ctt gcg gca acc ttc acc ctc atc ggt gtc tcc ttc	912
107	Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe	
108	290 295 300	
110	ttc gcg ctg cct gca ggc atc ttg ggg tct ggg ttt gcc ctg aag gtt	960
111	Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val	
112	305 310 315 320	
114	cag gag cag cac agg cag aag cac ttt gag aag agg cgg aac ccg gca	1008
115	Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala	
116	325 330 335	
118	gca ggc ctg atc cag tcg gcc tgg aga ttc tac gcc acc aac ctc tcg	1056
119	Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser	
120	340 345 350	
122	cgc aca gac ctg cac tcc acg tgg cag tac tac gag cga acg gtc acc	1104
123	Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr	
124	355 360 365	
126	gtg ccc atg tac agt tcg caa act caa acc tac ggg gcc tcc aga ctt	1152

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127	Val	Pro	Met	Tyr	Ser	Ser	Gln	Thr	Gln	Thr	Tyr	Gly	Ala	Ser	Arg	Leu	
128		370					375					380					
130	atc	ccc	ccg	ctg	aac	cag	ctg	gag	ctg	ctg	agg	aac	ctc	aag	agt	aaa	1200
131	Ile	Pro	Pro	Leu	Asn	Gln	Leu	Glu	Leu	Leu	Arg	Asn	Leu	Lys	Ser	Lys	
132	385					390					395					400	
134	tct	gga	ctc	gct	ttc	agg	aag	gac	ccc	ccg	ccg	gag	ccg	tct	cca	agt	1248
135	Ser	Gly	Leu	Ala	Phe	Arg	Lys	Asp	Pro	Pro	Pro	Glu	Pro	Ser	Pro	Ser	
136					405					410					415		
138	aaa	ggc	agc	ccg	tgc	aga	ggg	ccc	ctg	tgt	gga	tgc	tgc	ccc	gga	cgc	1296
139	Lys	Gly	Ser	Pro	Cys	Arg	Gly	Pro	Leu	Cys	Gly	Cys	Cys	Pro	Gly	Arg	
140				420					425					430			
142	tct	agc	cag	aag	gtc	agt	ttg	aaa	gat	cgt	gtc	ttc	tcc	agc	ccc	cga	1344
143	Ser	Ser	Gln	Lys	Val	Ser	Leu	Lys	Asp	Arg	Val	Phe	Ser	Ser	Pro	Arg	
144			435					440					445				
146	ggc	gtg	gct	gcc	aag	ggg	aag	ggg	tcc	ccg	cag	gcc	cag	act	gtg	agg	1392
147	Gly	Val	Ala	Ala	Lys	Gly	Lys	Gly	Ser	Pro	Gln	Ala	Gln	Thr	Val	Arg	
148		450				455					460						
150	cgg	tca	ccc	agc	gcc	gac	cag	agc	ctc	gag	gac	agc	ccc	agc	aag	gtg	1440
151	Arg	Ser	Pro	Ser	Ala	Asp	Gln	Ser	Leu	Glu	Asp	Ser	Pro	Ser	Lys	Val	
152	465				470					475					480		
154	ccc	aag	agc	tgg	agc	ttc	ggg	gac	cgc	agc	cgg	gca	cgc	cag	gct	ttc	1488
155	Pro	Lys	Ser	Trp	Ser	Phe	Gly	Asp	Arg	Ser	Arg	Ala	Arg	Gln	Ala	Phe	
156				485					490					495			
158	cgc	atc	aag	ggt	gcc	gcg	tca	cgg	cag	aac	tca	gaa	gaa	gca	agc	ctc	1536
159	Arg	Ile	Lys	Gly	Ala	Ala	Ser	Arg	Gln	Asn	Ser	Glu	Glu	Ala	Ser	Leu	
160			500					505				510					
162	ccc	gga	gag	gac	att	gtg	gat	gac	aag	agc	tgc	ccc	tgc	gag	ttt	gtg	1584
163	Pro	Gly	Glu	Asp	Ile	Val	Asp	Asp	Lys	Ser	Cys	Pro	Cys	Glu	Phe	Val	
164			515				520					525					
166	acc	gag	gac	ctg	acc	ccg	ggc	ctc	aaa	gtc	agc	atc	aga	gcc	gtg	tgt	1632
167	Thr	Glu	Asp	Leu	Thr	Pro	Gly	Leu	Lys	Val	Ser	Ile	Arg	Ala	Val	Cys	
168		530				535					540						
170	gtc	atg	cgg	ttc	ctg	gtg	tcc	aag	cgg	aag	ttc	aag	gag	agc	ctg	cgg	1680
171	Val	Met	Arg	Phe	Leu	Val	Ser	Lys	Arg	Lys	Phe	Lys	Glu	Ser	Leu	Arg	
172	545				550					555					560		
174	ccc	tac	gac	gtg	atg	gac	gtc	atc	gag	cag	tac	tca	gcc	ggc	cac	ctg	1728
175	Pro	Tyr	Asp	Val	Met	Asp	Val	Ile	Glu	Gln	Tyr	Ser	Ala	Gly	His	Leu	
176				565					570					575			
178	gac	atg	ctg	tcc	cga	att	aag	agc	ctg	cag	tcc	agg	caa	gag	ccc	cgc	1776
179	Asp	Met	Leu	Ser	Arg	Ile	Lys	Ser	Leu	Gln	Ser	Arg	Gln	Glu	Pro	Arg	
180			580					585				590					
182	ctg	cct	gtc	cag	cag	ggg	aca	aga	acg	ggg	tgg	gct	tct	ggg	aca	aag	1824
183	Leu	Pro	Val	Gln	Gln	Gly	Thr	Arg	Thr	Gly	Trp	Ala	Ser	Gly	Thr	Lys	
184			595				600					605					
186	ccc	act	gtg	gcc	cat	ggt	ggg	agt	gca	ggg	ggt	gtg	tgg	gcg	ggg	cct	1872
187	Pro	Thr	Val	Ala	His	Gly	Gly	Ser	Ala	Gly	Gly	Val	Trp	Ala	Gly	Pro	
188		610				615					620						
190	cct	ccc	cac	cca	cgt	cgg	cct	ctg	tca	gct	tct	ggt	gtg	tct	tca	caa	1920
191	Pro	Pro	His	Pro	Arg	Arg	Pro	Leu	Ser	Ala	Ser	Val	Val	Ser	Ser	Gln	

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192 625          630          635          640
194 agt ctg ttt taa
195 Ser Leu Phe
199 <210> SEQ ID NO: 2
200 <211> LENGTH: 643
201 <212> TYPE: PRT
202 <213> ORGANISM: Homo sapiens
204 <400> SEQUENCE: 2
206 Met Val Gln Lys Ser Arg Asn Gly Gly Val Tyr Pro Gly Pro Ser Gly
207 1          5          10          15
210 Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
211          20          25          30
214 Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
215          35          40          45
218 Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
219          50          55          60
222 Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
223 65          70          75          80
226 Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
227          85          90          95
230 Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
231          100         105         110
234 Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
235          115         120         125
238 Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
239          130         135         140
242 Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
243 145         150         155         160
246 Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
247          165         170         175
250 Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
251          180         185         190
254 Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
255          195         200         205
258 Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
259          210         215         220
262 Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
263 225         230         235         240
266 Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
267          245         250         255
270 Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
271          260         265         270
274 Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
275          275         280         285
278 Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
279          290         295         300
282 Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
283 305         310         315         320
286 Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala

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287          325          330          335
290 Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
291          340          345          350
294 Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
295          355          360          365
298 Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu
299          370          375          380
302 Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu Arg Asn Leu Lys Ser Lys
303 385          390          395          400
306 Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro Pro Glu Pro Ser Pro Ser
307          405          410          415
310 Lys Gly Ser Pro Cys Arg Gly Pro Leu Cys Gly Cys Cys Pro Gly Arg
311          420          425          430
314 Ser Ser Gln Lys Val Ser Leu Lys Asp Arg Val Phe Ser Ser Pro Arg
315          435          440          445
318 Gly Val Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala Gln Thr Val Arg
319          450          455          460
322 Arg Ser Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser Pro Ser Lys Val
323 465          470          475          480
326 Pro Lys Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala Arg Gln Ala Phe
327          485          490          495
330 Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu Glu Ala Ser Leu
331          500          505          510
334 Pro Gly Glu Asp Ile Val Asp Asp Lys Ser Cys Pro Cys Glu Phe Val
335          515          520          525
338 Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile Arg Ala Val Cys
339          530          535          540
342 Val Met Arg Phe Leu Val Ser Lys Arg Lys Phe Lys Glu Ser Leu Arg
343 545          550          555          560
346 Pro Tyr Asp Val Met Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu
347          565          570          575
350 Asp Met Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg Gln Glu Pro Arg
351          580          585          590
354 Leu Pro Val Gln Gln Gly Thr Arg Thr Gly Trp Ala Ser Gly Thr Lys
355          595          600          605
358 Pro Thr Val Ala His Gly Gly Ser Ala Gly Gly Val Trp Ala Gly Pro
359          610          615          620
362 Pro Pro His Pro Arg Arg Pro Leu Ser Ala Ser Val Val Ser Ser Gln
363 625          630          635          640
366 Ser Leu Phe
370 <210> SEQ ID NO: 3
371 <211> LENGTH: 1878
372 <212> TYPE: DNA
373 <213> ORGANISM: Homo sapiens
375 <220> FEATURE:
376 <221> NAME/KEY: CDS
377 <222> LOCATION: (1)..(1878)
379 <400> SEQUENCE: 3
380 atg gtg cag aag tcg cgc aac ggc ggc gta tac ccc ggc ccg agc ggg

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/519,335

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Input Set : N:\RJAVED\10519335.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:37; N Pos. 10,5363,8080,10296,14528,15336,15457,16288,16306,16307
Seq#:37; N Pos. 16316,16397,56012,57662
Seq#:37; N Pos. 60402,61110,98207,98208,98209,98210,98211,99743,108055
Seq#:37; N Pos. 109094,109125
Seq#:37; N Pos. 118900,119024,119025,119026,119027,119028,119029,119030
Seq#:37; N Pos. 119031,119032,119033,119034,119035,119036,119037,119038
Seq#:37; N Pos. 119039,119040,119041,119042,119043,119044,119045,119046
Seq#:37; N Pos. 119047,119048,119049,119050,119051,119052,119053,119054
Seq#:37; N Pos. 119055,119056,119057,119058,119059,119060,119061,119062
Seq#:37; N Pos. 119063,119064,119065,119066,119067,119068,119069,119070
Seq#:37; N Pos. 119071,119072,119073,119074,119075,119076,119077,119078
Seq#:37; N Pos. 119079,119080,119081,119082,119083,119084,119085,119086
Seq#:37; N Pos. 119087,119088,119089,119090,119091,119092,119093,119094
Seq#:37; N Pos. 119095,119096,119097,119098,119099,119100,119101,119102
Seq#:37; N Pos. 119103,119104,119105,119106,119107,119108,119109,119110
Seq#:37; N Pos. 119111,119112,119115,119116,119117,119118,119119,119120
Seq#:37; N Pos. 119121,119123,141674,142063,142137,142967,143077,143506
Seq#:37; N Pos. 143587,143629,149079

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32
Seq#:33,34,35,36,39,40,41,42,43,44,45,46,47

VERIFICATION SUMMARY

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Input Set : N:\RJAVED\10519335.txt

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L:1937 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
L:2121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:5314
L:2213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:8074
L:2287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:10294
L:2427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:14494
L:2455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:15334
L:2459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:15454
L:2485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:16234
L:2487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:16294
L:2489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:16354
L:3809 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:55954
L:3865 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:57634
L:3957 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:60394
L:3979 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:61054
L:5243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:98202
L:5303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:99719
L:5583 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:108053
L:5617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:109073
L:5943 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:118853
L:5947 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:118973
L:5949 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:119033
L:5951 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:119093
L:6725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:141615
L:6739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:142035
L:6741 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:142095
L:6769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:142935
L:6773 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:143055
L:6787 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:143475
L:6789 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:143535
L:6791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:143595
L:6979 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:149027